

Define Genes -----

```
Bmal1 <- new("gene",
  name="bmali",
  MGI="Arntl1",
  DDE="1",
  pars=c(bmali_d=.35),
  delay=4,
  boxin=c("RRE", "RRE"),
  boxout=c(""),
  boxouta=c("E-box"))
```

```
Reverba <- new("gene",
  name="reverba",
  MGI="Nr1d1",
  DDE="1",
  pars=c(reverba_d=.60),
  delay=1.2,
  boxin=c("E-box", "E-box", "E-box", "D-box"),
  boxout=c("RRE"),
  boxouta=c(""))
```

Define Boxes -----

```
Ebox <- new("box",
  name="E-box",
  inhibTerm="(in/(ikn+X))",
  actTerm="((an+avn*X)/(akn+X))")
```

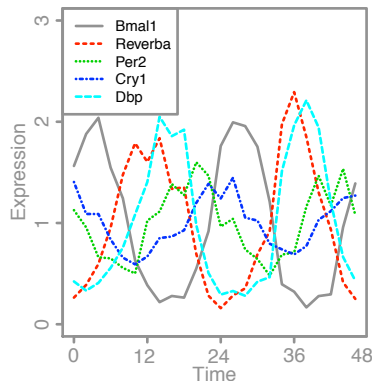
```
RRE <- new("box",
  name="RRE",
  inhibTerm="(in/(ikn+X))",
  actTerm="((an+avn*X)/(akn+X))")
```

```
Dbox <- new("box",
  name="D-box",
  inhibTerm="(in/(ikn+X))",
  actTerm="((an+avn*X)/(akn+X))")
```

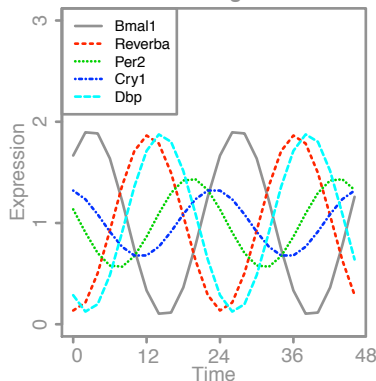
Define network from genes and boxes -----

```
rawnet <- new("network",
  name="korencic2gene",
  genes=c(Bmal1, Reverba),
  boxes=c(Ebox, Dbox, RRE))
```

Raw Experimental
Time Series Data



Experimental Data
Sinusoid Regression



Fitted Model

